

# Conor R. Walker

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## Education

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### University of Cambridge, UK

2017–2021

PhD in Computational Biology

- Thesis: Statistical analysis of short template switch mutations in human genomes
- Advisers: Nick Goldman, Aylwyn Scally, Nicola De Maio

### Newcastle University, UK

2016–2017

MSc Bioinformatics · first-class honours (83%)

- Thesis: Optimising nucleic acid sequences for DNA strand displacement systems
- Adviser: Harold Fellermann

### Liverpool John Moores University, UK

2013–2016

BSc (Hons) Zoology · first-class honours (80%)

- Thesis: The genetics of insecticide resistance in the blackfly *Simulium vittatum*
- Advisers: Craig Wilding, Will Swaney

## Research experience

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### New York Genome Center, USA

Jan. 2022–Present

Postdoctoral Research Associate · G<sup>2</sup> Lab

- I am leading research into privacy-preserving methods for analysing large-scale human functional genomics data. Joint appointment at Columbia University.

### Columbia University, USA

Jan. 2022–Present

Postdoctoral Research Associate

### European Bioinformatics Institute (EMBL-EBI), UK

2017–2022

Predocctoral Researcher

- I developed statistical methods to identify template switch variants in DNA sequences
- I characterised the human evolutionary, population, and cancer landscape of template switch mutagenesis
- I designed convolutional neural networks for accurately detecting between-species positive selection, validated through large-scale simulation of training and testing data

This work was funded by both EMBL and NIHR BRC.

### Newcastle University, UK

2016–2017

Postgraduate Student Research

- I implemented multi-objective genetic algorithms for designing and optimising DNA sequences for use in DNA computing systems

### Liverpool John Moores University, UK

2016

Undergraduate Student Research

- I identified enzyme families and point mutations associated with insecticide resistance in a medically-important blackfly genome using phylogenetic methods

## Publications

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### Peer-reviewed

phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets.

De Maio N., Boulton W., Weiguny L., Walker C. R., Turakhia Y., Corbett-Detig R., Goldman N.

[PLOS Computational Biology](#), 18, e1010056 (2022).

Mutation rates and selection on synonymous mutations in SARS-CoV-2.

De Maio N., [Walker C. R.](#), Turakhia Y., Lanfear R., Corbett-Detig R., Goldman N.

[Genome Biology and Evolution 13, evab087](#) (2021).

Short-range template switching in great ape genomes explored using pair hidden Markov models.

[Walker C. R.](#), Scally A., De Maio N., Goldman N.

[PLOS Genetics 17, e1009221](#) (2021).

Stability of SARS-CoV-2 phylogenies.

Turakhia Y., De Maio N., Thornlow B., Gozashti L., Lanfear R., [Walker C. R.](#), Hinrichs A. S., Fernandes J. D., Borges R., Slodkiewicz G., Weilguny L., Haussler D., Goldman N., Corbett-Detig R.

[PLOS Genetics 16, e1009175](#) (2020).

A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages.

Dellicour S., Durkin K., Hong S. L., Vanmechelen B., Martí-Carreras J., Gill M. S., Meex C., Bontems S., André E., Gilbert M., [Walker C. R.](#), De Maio N., Faria N. R., Hadfield J., Hayette M., Bours V., Wawina-Bokalanga T., Artesi M., Baele G., Maes P.

[Molecular Biology and Evolution 38, 1608–1613](#) (2020).

### Preprint/equivalent

Masking strategies for SARS-CoV-2 alignments.

De Maio N., [Walker C. R.](#), Borges R., Weilguny L., Slodkiewicz G., Goldman N.

[virological.org/t/masking-strategies-for-sars-cov-2-alignments/480](#) (2020).

Issues with SARS-CoV-2 sequencing data.

De Maio N., [Walker C. R.](#), Borges R., Weilguny L., Slodkiewicz G., Goldman N.

[virological.org/t/issues-with-sars-cov-2-sequencing-data/473](#) (2020).

## Selected presentations

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ISMB/ECCB 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

[Walker C. R.](#), De Maio N., Goldman N.

SMBE 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

[Walker C. R.](#), De Maio N., Goldman N.

SMBE 2019

Jul. 2019

Poster: Short template switches explain mutation clusters in the human genome

[Walker C. R.](#), De Maio N., Goldman N.

NIHR BRC Annual Research Day

Jul. 2018

Talk: Investigating short template switch mutations in humans and model organisms

[Walker C. R.](#)

Phylogroup XI

Mar. 2018

Talk: Short template switch events explain mutation clusters in the human genome

[Walker C. R.](#), Löytynoja A., Goldman N.

## Teaching

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### Students supervised

Fatma Rabia Fidan

2021

- Masters-level project: Identifying *de novo* template switch mutations in trios of human genomes

Shayesteh Arasti (co-advised with Nicola De Maio)

2021

- Masters-level project: Using convolutional neural networks to detect positive selection

|  |      |
|--|------|
| Viacheslav Vasilev (co-advised with Nicola De Maio)  | 2020 |
| <ul style="list-style-type: none"> <li>• Masters-level project: Using convolutional neural networks to detect positive selection</li> </ul>            |      |
| William Xu (co-advised with Nicola De Maio)  | 2020 |
| <ul style="list-style-type: none"> <li>• Masters-level project: Using convolutional neural networks to detect positive selection</li> </ul>            |      |
| <b>Teaching assistant</b>  |      |
| Medics to Coders · University of Cambridge, UK   | 2018 |
| <ul style="list-style-type: none"> <li>• I helped to deliver practical sessions on programming in Python at the School of Clinical Medicine</li> </ul> |      |

## Honours and awards

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|---|-----------|
| Best student talk   | May 2019  |
| <ul style="list-style-type: none"> <li>• Audience vote at the annual EMBL-EBI PhD Seminar Day</li> </ul>                              |           |
| Outstanding performance by a MSc Bioinformatics programme student   | Oct. 2017 |
| <ul style="list-style-type: none"> <li>• Awarded for achieving the highest overall grade on my master's degree programme</li> </ul>   |           |
| Zoology prize   | Sep. 2016 |
| <ul style="list-style-type: none"> <li>• Awarded for achieving the highest overall grade on my bachelor's degree programme</li> </ul> |           |

## Other scientific activities

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### Committees

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|--|-----------|
| Student Representative · EMBL-EBI, UK  | 2018–2020 |
| <ul style="list-style-type: none"> <li>• Attended meetings with senior management from across all EMBL outstations to discuss issues impacting the graduate community at EMBL</li> <li>• Organised a variety of academic and social events within the institution</li> </ul> |           |
| Graduate Student and Post-Doc Forum member · University of Cambridge, UK   | 2018      |
| <ul style="list-style-type: none"> <li>• I worked as part of a group of students and postdocs to devise strategies for creating a more positive experience for graduate students in the School of Life Sciences</li> </ul>   |           |

### Memberships

International Society for Computational Biology  
Society for Molecular Biology and Evolution  
Society for the Study of Evolution

### Reviewer for

Nature Medicine  
Molecular Biology and Evolution  
BMC Bioinformatics

## Skills

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|-----------------------------------|---|
| <b>Programming</b>                | Python, Bash, C++, R, AWK, LaTeX  |
| <b>Libraries</b>                  | Numpy, SciPy, Keras, TensorFlow, PyTorch, scikit-allel, matplotlib, seaborn, Scanpy |
| <b>Coding practices</b>           | Git, Snakemake, Nextflow, unit testing, Docker, Singularity, Jupyter, Vim           |
| <b>High performance computing</b> | LSF, Slurm  |
| <b>Operating systems</b>          | Linux, MacOS  |